

Result	No.	Score	Query Match	Length	DB	ID	Description
1	960	99.5	187	2	AA121991	AA121991 Human contig	
2	893	92.5	177	5	AAU76866	AAU76866 Human contig	
3	890	92.2	177	5	AAU76865	AAU76865 Human contig	
4	534	55.3	187	2	AA121592	AA121592 Human contig	
5	333.5	34.6	176	5	AB178916	AB178916 Human contig	
6	286.5	29.7	184	3	AA1823149	AA1823149 Human contig	
7	286.5	29.7	184	3	ABU071332	ABU071332 Human contig	
8	286.5	29.7	184	3	ABU071332	ABU071332 Human contig	
9	286.5	29.7	184	3	ABU071332	ABU071332 Human contig	
10	286.5	29.7	184	3	ABU071332	ABU071332 Human contig	
11	282.5	29.3	180	5	AB178376	AB178376 Human contig	
12	281.5	29.2	184	3	AA1823150	AA1823150 Human contig	
13	281.5	29.2	184	3	ABU071332	ABU071332 Human contig	
14	281.5	29.2	184	3	ABU071332	ABU071332 Human contig	
15	276.5	28.7	184	5	AAU76848	AAU76848 Human contig	
16	276.5	28.7	184	5	AAU76857	AAU76857 Human contig	
17	262	27.2	181	4	ABU52684	ABU52684 Human contig	
18	231	23.9	178	3	AA1808817	AA1808817 Human contig	
19	197.5	17.9	190	5	AB154907	AB154907 Human contig	
20	171	17.3	33	2	AA180232	AA180232 Human contig	
21	171	17.7	33	2	AB185558	AB185558 Human contig	
22	171	17.7	116	7	ABU52684	ABU52684 Human contig	
23	162.5	16.8	180	6	AA1823150	AA1823150 Human contig	
24	160.5	16.6	180	6	AA1823150	AA1823150 Human contig	
25	155.5	16.1	160	3	AA1808816	AA1808816 Human contig	

CC of therapeutic intervention in these cases. Inhibition of complement may  
 CC also be favorable in cases that involve tissue damage caused by vascular  
 CC injury such as myocardial infarction, cerebral vascular accidents or  
 CC acute shock lung syndrome. In these cases the complement system may  
 CC contribute to the destruction of partially damaged tissue as in  
 CC acute rejection of transplanted organs. In these cases the complement  
 CC system target specificities could reduce the activity of tissue damaging  
 CC proteins at sites of inflammation. Complement inhibition is important in  
 CC the prevention of xenograft rejection (the inhibition of complement by  
 CC cell-associated and soluble inhibitors is useful in protecting the  
 CC transplant from damage caused by activation of endogenous complement. The  
 CC present sequence represents the vWF domain of human factor MAC-1

XX Sequence 187 AA;  
 CC Query Match 99.5%; Score 950; DB 2; Length 187;  
 CC Best Local Similarity 100.0%; Pred. No. 1.4e-97;  
 CC Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CPQSDSDIAFLIDGSGSIIPHDFRMRKSFVSTVMEQLKSKTLPFLMYSSEFRIHFTFK 60  
 DB 1 CPQSDSDIAFLIDGSGSIIPHDFRMRKSFVSTVMEQLKSKTLPFLMYSSEFRIHFTFK 60  
 QY 61 EFQNNPNRSLVKPITOLLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 120  
 DB 61 EFQNNPNRSLVKPITOLLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 120  
 QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPDRHVFOVNNFE 180  
 DB 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPDRHVFOVNNFE 180  
 QY 181 IQNQLRE 187  
 DB 181 IQNQLRE 187

RESULT 2  
 AAU76866  
 ID AAU76866 standard; protein; 177 AA.  
 AC AAU76866;  
 DT 21-MAY-2002 (first entry)  
 XX Human integrin alpha subunit CD11b deletion variant A domain #2.  
 XX Human; Integrin alpha subunit; A domain; CD11b; integrin beta subunit;  
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;  
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;  
 KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;  
 XX mutain.  
 OS Homo sapiens.  
 XX Synthetic.

XX Key Location/Qualifiers  
 XX Key Location/Qualifiers  
 FT Misc-difference 172  
 FT Misc-difference 177 /note= "Wild-type Val substituted by Cys"  
 FT Misc-difference 177 /note= "Wild-type Ala substituted by Cys"  
 XX W0200209737-A1.  
 XX  
 PD 07-FEB-2002.  
 XX  
 XX 31-JUL-2001; 2001WO-US023957.  
 XX  
 XX 31-JUL-2000; 2000US-0221950P.  
 PR 11-JAN-2001; 2001US-00758493.  
 PR 13-MAR-2001; 2001US-00805354.  
 XX  
 XX (GEO) GEN HOSPITAL CORP.

PI Arnaout AM, Li R, Xiong J;  
 XX WPI; 2002-186697/24.  
 XX Novel high affinity integrin polypeptide useful for treating restenosis  
 XX and parasitic diseases, comprises all or part of variant integrin alpha  
 XX subunit A domain or variant integrin beta subunit A-like domain.

XX Claim 21; Page: 55pp; English.  
 CC The invention relates to a high affinity integrin polypeptide comprising  
 CC all or part of a variant integrin alpha subunit A domain or a variant  
 CC integrin beta subunit A-like domain. The polypeptide, preferably, is  
 CC CD11b alpha subunit A-like domain. The residue 320 have been replaced by  
 CC C, or G, or A, or T, or C, or G, or A, or T, or C, or G, or A, or T, or C, or  
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful  
 CC for determining if a test compound is a candidate compound for binding to  
 CC CD11b or for treating an inflammatory disorder, by contacting a test  
 CC compound with the polypeptide and determining if the test compound binds  
 CC to the polypeptide. The integrin subunits are useful for reducing  
 CC skeletal muscle injury, for treating disorders caused by ischaemia-  
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,  
 CC to purify variant integrin polypeptide ligands and as bait proteins in  
 CC two-hybrid or three-hybrid assays. This sequence represents a human  
 CC integrin alpha subunit A-like domain deletion variant A domain. Note: This  
 CC sequence is not featured in the specification but has been  
 CC derived from the wild-type protein shown in AAU76847

XX Sequence 177 AA;  
 CC Query Match 92.5%; Score 893; DB 5; Length 177;  
 CC Best Local Similarity 97.7%; Pred. No. 3.4e-90;  
 CC Matches 172; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CPQSDSDIAFLIDGSGSIIPHDFRMRKSFVSTVMEQLKSKTLPFLMYSSEFRIHFTFK 60  
 DB 1 CPQSDSDIAFLIDGSGSIIPHDFRMRKSFVSTVMEQLKSKTLPFLMYSSEFRIHFTFK 60  
 QY 61 EFQNNPNRSLVKPITOLLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 120  
 DB 61 EFQNNPNRSLVKPITOLLGRTHTATGIRKRVRELFINITNGARKNAFKILVITDGEKFG 120  
 QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPDRHVFOVNNFE 176  
 DB 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPDRHVFOVNNFE 176

RESULT 3  
 AAU76865  
 ID AAU76865 standard; protein; 177 AA.  
 AC AAU76865;  
 DT 21-MAY-2002 (first entry)  
 XX Human integrin alpha subunit CD11b deletion variant A domain #1.  
 XX Human; Integrin alpha subunit; A domain; CD11b; integrin beta subunit;  
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;  
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;  
 KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;  
 XX mutain.  
 OS Homo sapiens.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 170  
 FT Misc-difference 177 /note= "Wild-type Phe substituted by Cys"  
 FT Misc-difference 177 /note= "Wild-type Ala substituted by Cys"  
 XX W0200209737-A1.





CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs  
 CC to active agents; and (v) for affinity chromatography. The Ab  
 CC retain about the same activities in which they are derived. The response  
 CC assays as the murine antibodies from which they are derived. The murine  
 CC anti-CD11a antibody MH24 has IC50 0.09 nM for preventing adhesion  
 CC between Jurkat cells (expressing LFA-1) and normal epidermal  
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).  
 CC The fully humanized version of MH24 had IC50 0.13 nM. The present  
 CC sequence represents the amino acid sequence of the human CD11a I-domain,  
 CC which is used in the exemplification of the present invention  
 XX  
 XQ Sequence 184 AA;

Query Match 29.7%; Score 286.5; DB 3; Length 184;  
 Best Local Similarity 33.5%; Pred. No. 4,7e-23;  
 Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;  
 QY 7 DIAPLIDSGSIIPHDPRMKEFVSTVMEOLKSKTLFSLMOYSEFRHFTKFPQNP 66  
 DB 5 DLVFLDGSNLSQDFQKILDPKMKVKKLSNTSYQAAVQSTYKTFDFSDYVKR 64  
 QY 67 NPSRLVPTOLLGRTHFATGIRKVRLEPNTNGARKNAFKILVITDGSKFGDPLGYE 126  
 DB 65 DPDLALHGVKMLLNTFGALVYATVEFRELGARPDATKLVIIITDGE--ATDSGNI 122  
 QY 127 DVIPEADREGVIRYVGVDPAFSEKSGRELNTIASKPPDHVFOVNFALKTIONOLR 186  
 DB 123 DAAND-----IIRYIIGIGKHQFOTKESQETLHKFASKPASEFVKILDTFELKDLTFLQ 177  
 QY 187 EK 188  
 DB 178 KK 179

RESULT 7  
 ABU07332  
 ID ABU07332 standard; protein; 184 AA.  
 AC ABU07332;  
 XX  
 XX 29-JAN-2003 (first entry)  
 XX  
 XX Human expressed protein tag (EPT) #2033.  
 XX  
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 XX protease; process inhibitor; transporter; cytoskeletal protein;  
 XX major histocompatibility complex; melanoma; lymphoma; leukemia;  
 XX adenocarcinoma; sarcoma; melanoma, lymphoma, leukemia.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200278524-A2.  
 XX  
 XX 10-OCT-2002.  
 XX  
 XX 28-MAR-2002; 2002WO-US009671.  
 XX  
 XX 28-MAR-2001; 2001US-0279495P.  
 XX  
 XX 21-MAY-2001; 2001US-0292544P.  
 XX  
 XX 08-AUG-2001; 2001US-0310801P.  
 XX  
 XX 01-OCT-2001; 2001US-0326370P.  
 XX  
 XX 04-DEC-2001; 2001US-0336780P.  
 XX  
 XX 20-FEB-2002; 2002US-0358985P.  
 XX  
 XX (ZYCO-) ZYCO INC.  
 XX  
 XX Chicz RM, Tomlinson AJ, Urban RG;  
 XI  
 XX WPI; 2003-040607/03.  
 XX  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 XX cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 XX Example 2; SEQ ID NO 2033; 134pp; English.  
 XX  
 XX The invention describes a purified polypeptide, which comprises a  
 XX fragment of a kinase, phosphatase, protease, or protease inhibitor.  
 XX transporter, cytoskeletal protein, receptor or transcription factor. The  
 XX polypeptide is useful as an immunogenic composition for eliciting in a  
 XX mammal an immunogenic response directed against any of the purified  
 XX polypeptide. The purified polypeptide, or the antibody that binds to this  
 XX polypeptide, is useful for treating cancer. The polypeptide is also  
 XX useful for identifying compounds that binds to a naturally processed  
 XX epitope of a naturally occurring polypeptide. The polypeptides and  
 XX polynucleotides are useful for treating cancer, sarcoma, melanoma,  
 XX lymphoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, and  
 XX leukemia or leukaemia. These are also useful for screening agents for  
 XX treating the above mentioned diseases. This sequence represents an  
 XX expressed protein tag (EPT) isolated from human tissue for translational  
 XX profiling. Note: This sequence does not appear in the printed  
 XX specification but was obtained in electronic format directly from WIP0 at  
 XX ftp.wipo.int/pub/published\_pct\_sequences

Query Match 29.7%; Score 286.5; DB 6; Length 184;  
 Best Local Similarity 33.5%; Pred. No. 4,7e-23;  
 Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;  
 QY 7 DIAPLIDSGSIIPHDPRMKEFVSTVMEOLKSKTLFSLMOYSEFRHFTKFPQNP 66  
 DB 5 DLVFLDGSNLSQDFQKILDPKMKVKKLSNTSYQAAVQSTYKTFDFSDYVKR 64  
 QY 67 NPSRLVPTOLLGRTHFATGIRKVRLEPNTNGARKNAFKILVITDGSKFGDPLGYE 126  
 DB 65 DPDLALHGVKMLLNTFGALVYATVEFRELGARPDATKLVIIITDGE--ATDSGNI 122  
 QY 127 DVIPEADREGVIRYVGVDPAFSEKSGRELNTIASKPPDHVFOVNFALKTIONOLR 186  
 DB 123 DAAND-----IIRYIIGIGKHQFOTKESQETLHKFASKPASEFVKILDTFELKDLTFLQ 177  
 QY 187 EK 188  
 DB 178 KK 179

RESULT 8  
 ABU07332  
 ID ABU07332 standard; protein; 184 AA.  
 AC ABU07332;  
 XX  
 XX 26-FEB-2004 (first entry)  
 XX  
 XX Human CD11a I-domain.  
 XX  
 XX Human; CD11a; I-domain; monoclonal antibody;  
 XX Cluster of differentiation 11a; mixed lymphocyte response assay;  
 XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;  
 XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;  
 XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;  
 XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
 XX diabetes mellitus; prodrug activating enzyme.  
 XX  
 XX Homo sapiens.  
 XX  
 XX US2003207336-A1.  
 XX  
 XX 06-NOV-2003.  
 XX  
 XX 28-FEB-2001; 2001US-00795798.  
 XX  
 XX 27-NOV-1996; 96US-0031971P.



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SQ Sequence 184 AA;
Query Match 29.7%; Score 286.5; DB 8; Length 187;
Best Local Similarity 33.0%; Pred. No. 4, 8e-23;
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;
OY 7 DIAFLDGGSGIIIPHDPRMKEFVSTVMEQLKKSTLPSLMQYSEPRHPTFK 66
DB 5 DLVFLFDGSGMSLQDFKILDMKDKVKKLSNTSYQFAAVQFSTSYKTEFDFSDYVKR 64
OY 67 WPSRLVKEITOLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFDPLGYE 126
DB 65 DPVALGKRVHLLNTYTGAINVATEVFRLELGPDPKATKVLIIITDGE--ATDSGNI 122
OY 127 DPLGVDPADREGVIRVIGVDAPRSEKRSQBLNTIASKPRDRHVPQNNPEALKT 186
DB 123 DAAKD-----IIRIIGIKGHTQKESQETLHKFASKPASEVKILDTFEKLDPTELQ 177
OY 187 KK 188
DB 178 KK 179

RESULT 10
ADR23224
ID ADR23224 standard; protein; 187 AA.
XX AC ADR23224;
XX DT 04-NOV-2004 (first entry)
XX DE Human integrin CD11a alpha subunit A domain.
XX KW Human; integrin; CD11a; inflammation; antiinflammatory; vasotropic.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX PM Domain 1..184
XX FT /label = A_domain
XX FT Misc-difference 182
XX FT "Invariant Ile residue"
XX WO2004066914-A2.
XX PD 12-AUG-2004.
XX PR 12-MAY-2003; 2003WO-US014919.
XX PR 10-MAY-2002; 2002US-0014259.
XX PA (GSHO ) GEN HOSPITAL CORP.
XX PI Arnaud M, Li R, Xiong J;
XX WIPI; 2004-593980/57.
XX GENBANK; AAC31672.
XX Novel variant integrin CD11b alpha subunit polypeptide, useful for
XX determining candidate compound for binding to CD11b, and for determining
XX compound as activation-dependent ligand.
XX PS Disclosure; SEQ ID NO 4; 128pp; English.
XX The present sequence is that of the human integrin alpha subunit CD11a A
XX domain (amino acids 150-333 of the full-length protein). This includes an
XX invariant Ile residue. The invention features variant integrin alpha
XX subunit polypeptides in which the invariant Ile is substituted by Gly,
XX Ala or some other amino acid (e.g. Val) or is deleted. The polypeptide
XX can include part or all of the A domain. Replacing the invariant Ile
XX creates a variant integrin polypeptide that is more active (i.e. in
XX structure, a greater proportion of ligand forming polypeptides than
XX the wild-type form of the subunit. Variant integrin polypeptides of the
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CC invention are useful in assays for compounds that bind to a variant
CC ligand, that interfere with or enhance the binding of an integrin ligand
CC to integrin, and for identifying activation-specific ligands. They are
CC also useful for generating antibodies, e.g. monoclonal antibodies, which
CC stand to the high efficiency form of an integrin. Some such antibodies
CC are described in the present invention. The invention also provides
CC integrin that is in a lower affinity conformation. The invention also
CC provides methods of administering a variant integrin polypeptide, or an
CC antibody that selectively binds it, to identify a ligand which binds to
CC an active integrin. Such assays are useful for diagnosing inflammation,
CC e.g. occult inflammation (e.g. abscess or an active arteriosclerotic
CC lesion). Variant integrin polypeptides can also be used to affect the
CC bioavailability of a variant integrin polypeptide ligand and to treat
CC disorders associated with aberrant or unwanted integrin expression or
CC activity, such as vascular injury. A variant CD11a A domain containing an
CC dependent ligand (ICAM-1 in an ELISA assay). No binding was observed to the
CC wild-type protein. Claimed polypeptides comprise: amino acids 150-331 of
CC the CD11a alpha subunit sequence in which the Ile residue at position 331
CC is replaced by Gly or Ala; and amino acids 150-330 of the CD11a alpha
CC subunit but not amino acids 331-1223 of CD11a.
XX
XX SQ Sequence 187 AA;
Query Match 29.7%; Score 286.5; DB 8; Length 187;
Best Local Similarity 33.0%; Pred. No. 4, 8e-23;
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;
OY 1 CPQSDIAFLDGGSGIIIPHDPRMKEFVSTVMEQLKKSTLPSLMQYSEPRHPTFK 60
DB 1 CIKGNVLVFLFDGSGMSLQDFKILDMKDKVKKLSNTSYQFAAVQFSTSYKTEFDF 60
OY 61 EFQNNPRLSLVKEITOLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
DB 61 DYVKKDPDALLGVHMLLNTYTGAINVATEVFRLELGPDPKATKVLIIITDGE--A 118
OY 121 DPLGVDPADREGVIRVIGVDAPRSEKRSQBLNTIASKPRDRHVPQNNPEALKT 180
DB 119 TDSGVIDAKD-----IIRIIGIKGHTQKESQETLHKFASKPASEVKILDTFEKL 173
OY 181 IONOLREK 188
DB 174 LFTLEQKK 181

RESULT 11
ABR76376
ID ABR76376 standard; protein; 180 AA.
XX AC ABR76376;
XX DT 22-AUG-2002 (first entry)
XX DE Lymphocyte function associated antigen-1 I domain.
XX KW Lymphocyte function associated antigen-1; LFA-1; human;
XX OS Homo sapiens.
XX PM WO2002021511-A2.
XX PD 18-APR-2002.
XX PF 12-OCT-2001; 2001WO-US032047.
XX PR 12-OCT-2000; 2000US-0239750P.
XX PA (ICOS-) ICOS CORP.
XX ST Staton DE;
XX WIPI; 2002-471361/50.
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XX Modulating binding interactions between alpha/beta proteins comprising  
PT allosteric regulatory sites, and a binding partner, by contacting with an  
PT allosteric effector molecule that interacts with the regulatory site.  
XX  
XX Disclosure; Fig 1; 163pp; English.

XX The present sequence is the protein sequence of the integrin (I) domain  
CC of lymphocyte function associated antigen-1 (LFA-1). The invention  
CC provides methods of modulating the binding interaction of a first  
CC molecule, which is not LFA-1 or an I domain-containing fragment of LFA-1,  
CC and a binding partner. The first molecule has an alpha/beta domain  
CC structure comprising an allosteric regulatory site. Modulation of the  
CC binding interaction involves contacting with an allosteric effector  
CC molecule that interacts with the regulatory site. In vivo methods are  
CC expected to alter and/or prevent pathological states arising from  
CC aberrant binding activity. Methods for identifying modulators are also  
CC provided.

XX Sequence 180 AA;

Query Match 29.3%; Score 282.5; DB 5; Length 180;  
Best Local Similarity 33.5%; Pred. No. 1.3e-22;  
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAPLIDSGSIIHDFPRMKEFVSTYNEOLKKSKTFLSLMOYSSEFRIHPTFKFQNP 66  
Db 4 DLVFLDGSNSLQDFEQKILDPKDWKKLSNTSYQFAVQFSTYKTEFDSFYVK 63

Qy 67 NPRLVXPITOLLGRTHATGIRKVVRELNTNGARKNAPKILVVITDGEKFGDPLGYE 126  
Db 64 DPDLLEHVKHMLLNTFGAINVYATEVFRELGPDPATKVLIIITDGS--ATDSGNI 121

Qy 127 DVIPADREGVIRYVGVDAPRSEKRSQSLMTASKPPRDHVFQVNNFEALKTIONQLR 186

Db 122 DAAKD-----IIRYIIGIGHFQTKESQETLHKFASKPASEFVKILDTFEKLDFELQ 176

Qy 187 EK 188

Db 177 KK 178

RESULT 12

AAV82350

ID AAV82350 standard; protein; 184 AA.

AC AAV82350;

DT 22-JUN-2000 (first entry)

XX Rheus CD11a I-domain amino acid sequence SEQ ID NO:8.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;

XX antitumour; antiviral; inflammation; immunological response; LFA-1;

XX lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;

XX inflammatory bowel disease; systemic lupus erythematosus; leukaemia;

XX viral infection; transplant rejection; graft rejection.

XX Macaca mulatta.

XX US6037454-A.

XX 14-MAR-2000.

XX 20-NOV-1997; 97US-00974899.

XX 27-NOV-1996; 96US-0031971P.

XX (GETH ) GRNENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.  
PT inflammation and transplant rejection, contains human heavy variable  
PT region complementarity determining regions.

XX Example; Fig 2; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that  
CC binds specifically to the human CD11a I-domain. The Ab has anti-  
CC inflammatory, immunosuppressant, antitumour and antiviral activities. The  
CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is  
CC involved in leucocyte adhesion associated with inflammatory and  
CC immunological responses. The Ab are used: (i) optionally when coupled to  
CC a cyclosporin, to treat or prevent allograft rejection; (ii) optionally  
CC in combination with cyclosporin, to treat or prevent diseases such as  
CC psoriasis, leukaemia, viral infections and many others, also for  
CC inhibiting graft rejection; (iii) when labeled, to detect CD11a; (iii) for  
CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs  
CC to active anticancer agent; and (v) for affinity chromatography. The Ab  
CC retain about the same activity in adhesion and mixed lymphocyte response  
CC assays as the murine antibodies from which they are derived. The murine  
CC anti-CD11a antibody MPM24 has IC50 0.09 nM for preventing adhesion  
CC between Jurkat cells (expressing LFA-1) and normal epidermal leucocyte-1.  
CC The fully humanised antibody MPM24 has IC50 0.13 nM. The present  
CC sequence represents the amino acid sequence of the rheus CD11a I-domain,  
CC which is used in the exemplification of the present invention

XX Sequence 184 AA;

Query Match 29.2%; Score 281.5; DB 3; Length 184;  
Best Local Similarity 33.0%; Pred. No. 1.7e-22;  
Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAPLIDSGSIIHDFPRMKEFVSTYNEOLKKSKTFLSLMOYSSEFRIHPTFKFQNP 66  
Db 5 DLVFLDGSNSLQDFEQKILDPKDWKKLSNTSYQFAVQFSTYKTEFDSFYVK 64

Qy 67 NPRLVXPITOLLGRTHATGIRKVVRELNTNGARKNAPKILVVITDGEKFGDPLGYE 126  
Db 65 DPDLLEHVKHMLLNTFGAINVYATEVFRELGPDPATKVLIIITDGS--ATDSGNI 122

Qy 127 DVIPADREGVIRYVGVDAPRSEKRSQSLMTASKPPRDHVFQVNNFEALKTIONQLR 186  
Db 123 DAAKD-----IIRYIIGIGHFQTKESQETLHKFASKPASEFVKILDTFEKLDFELQ 177

Qy 187 EK 188

Db 178 KK 179

RESULT 13

ADG38996

ID ADG38996 standard; protein; 184 AA.

AC ADG38996;

DT 26-FEB-2004 (first entry)

XX Monkey CD11a I-domain.

XX Monkey; CD11a; I-domain; monoclonal antibody;

XX cluster of differentiation 11a; mixed lymphocyte response assay;

XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;

XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;

XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;

XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;

XX diabetes mellitus; prodrug activating enzyme.

XX Macaca mulatta.

XX US2003207336-A1.





disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is Rheus macaque CD11a I-domain protein. This sequence is used in the exemplification of the invention.

Sequence 184 AA;

Query Match 29.2%; Score 281.5; DB 8; Length 184;  
Best Local Similarity 33.0%; Pred. No. 1.7e-22;  
Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;

Oy 7 DIAPLDGSGIIIPDPRMKEFVSTVNEOLKSKTLFSLQVSEFRHFTFKFQNNP 66

Db 5 DLIFPDGSGSQPDEPKILDPKQVKKLNTSYQPNVQFSYKTEFDFSDYKOK 64

Oy 67 NPRLVKEITVOLLGRTHATGIRKVVRELENTNGARKNAFKLVITDGEKQDPIGYE 126

Db 65 DPDALEHVKMLLTNTFGAINVYVATEVPRELGAQPDATKVLIIITDGE--ATDSGNI 122

Oy 127 DVIPEDREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDRHVFQNNFEALKTQNL 186

Db 123 DAARD-----IIRVIIGIKGFQTKESQETLHKFPASBPVKILDTFEKLDPELQ 177

Oy 187 EK 188

Db 178 KK 179

RESULT 15

AAU76848

ID AAU76848 standard; protein; 184 AA.

XX AC AAU76848;

XX DT 21-MAY-2002 (first entry)

XX DE Human integrin alpha subunit CD11a A domain.

XX HU Human; integrin alpha subunit; A domain; CD11a; integrin beta subunit;

XX KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;

XX KW ischaemia-reperfusion injury; immune complex; parasitic disease;

XX KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Region 1..181

XX FT /note= "This region is specifically claimed"

XX WO200209737-A1.

XX PD 07-FEB-2002.

XX PP 31-JUL-2001; 2001WO-US023957.

XX PR 31-JUL-2000; 2000US-0221950P.

XX PR 11-JAN-2001; 2001US-00758493.

XX PR 13-MAR-2001; 2001US-00805354.

XX XX (GENO ) GEN HOSPITAL CORP.

XX XX Arnaout AM, Li R, Xiong J;

XX XX WPI; 2002-188687/24.

XX DR Novel high affinity integrin polypeptide useful for treating restenosis

XX PT and parasitic diseases, comprises all or part of variant integrin alpha

XX PT subunit A domain or variant integrin beta subunit A-like domain.

XX PS Example 2; Fig 5; 55pp; English.

XX CC The invention relates to a high affinity integrin polypeptide comprising

all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where the residue 32 has been replaced by V or A, residue 33 and residue 34 have been replaced by C or G, or residue 32 and residue 33 have been replaced by C, is useful for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, immune complexes, restenosis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents the human integrin alpha subunit CD11a A domain

Sequence 184 AA;

Query Match 28.7%; Score 276.5; DB 5; Length 184;  
Best Local Similarity 33.0%; Pred. No. 6e-22;  
Matches 62; Conservative 48; Mismatches 71; Indels 7; Gaps 2;

Oy 1 CPQEDSDIAPLDGSGIIIPDPRMKEFVSTVNEOLKSKTLFSLQVSEFRHFTFK 60

Db 1 CIKGNVDFLPDGSMSQDPDEPKILDPKQVKKLNTSYQPNVQFSYKTEFDF 60

Oy 61 EPNQNPBSLVKVIITOLLGRTHATGIRKVVRELENTNGARKNAFKLVITDGEKFG 120

Db 61 DYYKWDPDALLKHVKHMLLTNIFGAINVYVATEVPRELGAQPDATKVLIIITDGE--A 118

Oy 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDRHVFQNNFEALKT 180

Db 119 TDSGNIDAARD-----IIRVIIGIKGFQTKESQETLHKFPASBPVKILDTFEKLD 173

Oy 181 IQNLREK 188

Db 174 LPTLQKK 181

Search completed: November 14, 2005, 17:34:35

Job time : 165 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2005, 17:08:58 / Search time 38 Seconds  
(without alignments)  
476.020 Million cell updates/sec

Title: US-09-758-493-1\_COPY\_1\_188

Perfect score: 965

Sequence: 1 CPQEDSDIAFLDGGSGIIP.....VFQVNFPAKLTIONLAEK 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 95191

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: piri:\*

2: piri2:\*

3: piri3:\*

4: piri4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	81	8.4	170	B53274	complement factor
2	78.5	8.1	166	JT0358	hypothetical prote
3	73.5	7.5	187	A83255	hypothetical prote
4	71.5	7.4	169	B70474	ribosomal protein
5	71.5	7.4	169	B70474	hypothetical prote
6	70.5	7.3	181	G64307	hypothetical prote
7	70.5	7.3	187	AF0255	probable phage pro
8	69.5	7.2	141	A82880	ribosomal protein
9	69.5	7.2	146	H97788	hypothetical prote
10	68.5	7.1	90	H69159	hypothetical prote
11	67.5	7.0	172	I38424	centrin - human
12	67.5	7.0	175	A64330	hypothetical prote
13	67	6.9	150	C71706	hypothetical prote
14	66	6.9	171	A98901	uncharacterized co
15	66	6.9	176	A64330	hypothetical prote
16	65.5	6.8	152	G54553	hypothetical prote
17	65.5	6.8	172	G38531	uncharacterized co
18	65.5	6.8	180	C90526	conserved hypothet
19	65	6.7	132	PMPEL	H+-transporting tw
20	65	6.7	135	A84021	modulation of CheA
21	65	6.7	164	T10726	calmodulin - green
22	65	6.7	172	AH2456	hypothetical prote
23	64.5	6.7	150	1 MORTA2	myosin alkali ligh
24	64.5	6.7	159	2 AC2254	hypothetical prote
25	63.5	6.6	120	A64435	hypothetical prote
26	63.5	6.6	158	C93847	probable transmem
27	63.5	6.6	158	C93847	probable transmem
28	63.5	6.6	165	G81324	acylate catabolis
29	63	6.5	127	B70022	

#### ALIGNMENTS

##### RESULT 1

B53274

Complement factor B subunit Bb - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-May-2004

C:Accession: B53274

C:Protein: B53274 Van de Veghe, A.R.; Coppeters, W.R.; Van Zeveren, A.J.; Bouquet, Y.

C:Immunogenetics 34, 192-195, 1991

A:Title: Cloning and sequencing of the porcine complement factor B.

A:Reference number: A53274; MUID:91372866; PMID:1680099

A:Accession: B53274

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-170 <PEE>

A:Note: sequence extracted from NCBI backbone (NCBI:56036, NCBI:P.56043)

C:Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology

Query Match 8.4%; Score 81; DB 2; Length 170;

Best Local Similarity 22.0%; Pred. No. 7.7; Indels 38; Caps 8;

Matches 38; Conservative 33; Mismatches 38; Indels 38; Caps 8;

Qy 41 KTLFLMOYSEERFIHFTKEFQNNPNSL-VKPIITQLG-----RHTATGIRKV 92

Db 7 KPYGLVTVATDPKVLIRVS-----NPKSADADWVTEQLDKISYDDHKLKAGTNTKAL 60

Qy 93 RELFNTNGARKN-----AFKLWITDG--EKFGDPLGYEDVPEADREGVIR---- 139

Db 61 LEVYNNMGVNPFPNNTRHVLITDLNMGDSVTVIDRLNLNGDKRNP 120

Qy 140 -----YVIGVDGAFSEKSEKROELNTASKPRD--HFQVNNPRAKLTIONOL 185

Db 121 EDYLDIYVGVGVLNVQNE---NINALASKKXEQVFKLQVDNLSDVFFQM 169

##### RESULT 2

JT0358

hypothetical protein g6 (rep 3', region) - Clostridium perfringens plaamid pIP404

C:Species: Clostridium perfringens

C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C:Accession: JT0358

C:Protein: JT0358 S.T.

C:Immunogenetics 19, 134-150, 1988

A:Title: Complete nucleotide sequence and genetic organization of the bacteriocinogen

A:Reference number: JT0353; MUID:88336297; PMID:2901768

A:Accession: JT0358

A:Molecule type: DNA

A:Residues: 1-166 <GAR>

A:Cross-references: UNIPROT:P18017; GB:M32882; GB:J03309; NID:g150738; PIDN:AAA98252..

C:Genetic:

A:Genome: plasmid

Query Match 8.1%; Score 78.5; DB 2; Length 166;

A. Cross-references: UNIPROT: Q27130; GB: AE000876; GB: AE000666; NID: g5622140; PID: AAB

B. Experimental source: strain Delta H

C. Genes:   
A:   
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do:   
dp:

DB 103 PREETRIKYGG-IGVQVAVDISPQRVDLSLGPTTRGNAQAAPFKKXISBE 153

RESULT 5

B70474: Nucleic acid sequence  
C.Species: Aquifex aeolicus  
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C.Accession: B70474  
R.Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Graham, D.E.; V.  
Nature 392, 353-358, 1998  
Article: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A.Accession: B70474  
A.Creation: B70474  
A.Status: preliminary; nucleic acid sequence not shown; translation not shown  
A.Molecule type: DNA  
A.Residues: 1-169 <AQ>  
A.Cross-references: UNIPROT:Q67822; GB:AE000768; GB:AE0084249; PIDN:AA01  
A.Experimental source: strain VF5  
C.Genetic: 2028  
C.Superfamily: Archaeoglobus hypochemical protein AF1244

[illegible]

QY 121 DPLGVGVDEIPKAD-----REGVIRVYGVGD 146  
          ||:|          ||:|:|  
DB 134 SPDPEYKEIKQAGDTLLVVGTRBQLKEFMCGD 166

RESULT 6

G64307

hypothetical protein U00063 - Methanococcus jannaschii

C-Species: Methanococcus jannaschii

C-Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

R-Accession: G64307

R-Build: C01; White, O.; Olson, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overton, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glodek, S.; Adams, J.; Nelson, K.; Hama, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Staden, J. 973 1058-1073, 1996

A-Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. Authors: Kaine, B.P.; Borodovsky, M.; Klank, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R. 1996

C:\Program Files\Microsoft Office\Office11\Word\Word.exe

C:\Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 12-Jun-2003

55 QNKSTPASUFEPHTSLKDI AHKEAA - RSVIKHLEKVT - ADQAKYKELIIVAE PQMLG 110

469159  
 469159  
 Species: *Methanobacterium thermoautotrophicum* (strain Delta H)  
 Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 Accession: H69159  
 Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.

; Qiu, D.; Spadafora, R.; Vicalire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
 A:Reference number: A69000; MUID:98037514; PMID:9371463  
 A:Accession: H69159  
 A:Molecule type: DNA  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Residues: 1-90 <MTH>  
 A:Cross-references: UNIPROT:O26558; GB:AE000830; GB:AE000666; NID:g2621523; PIDN:AAB8496  
 A:Experimental source: strain Delta H  
 C:Genetics:  
 A:Gene: MTH458

Query Match 7.1%; Score 68.5; DB 2; Length 90;  
 Best Local Similarity 23.8%; Pred. No. 41;  
 Matches 24; Conservative 16; Mismatches 30; Indels 31; Gaps 5;

Qy 1 CPQSDIAFLDGGSGIIPHDPRKPEFVSTWEOQKKSTLFLSMQYSEFRHPTFK 60  
 Db 13 CDAEDRTV-----GATEIL-----RQVDTYET-KEKLRSQNYEAL----- 49

Qy 61 EPQNNPNSLVKPIITOLLGTHATGIRKVRLEFNITNG 101  
 Db 50 --FENRATP-----TAITDREWNITGNVRELFOVDEG 82

RESULT 11  
 138424 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
 C:Accession: 138424  
 R:Errabolu, R.; Sanders, M.A.; Salisbury, J.L.  
 J. Cell Sci. 107, 9-16, 1994  
 A:Title: Cloning of a cDNA encoding human centrin, an EF-hand protein of centrosomes and  
 A:Reference number: 138424; MUID:94230620; PMID:8175926  
 A:Accession: 138424  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-90 <KFS>  
 A:Cross-references: UNIPROT:Q12798; EMBL:U01270; NID:g3337234; PIDN:AC27343.1; PID:g414  
 A:Experimental source: strain  
 C:Superfamily: calmodulin; calmodulin repeat homology  
 C:Keywords: EF hand  
 P:28-60/Domain: calmodulin repeat homology <EF1>  
 P:64-96/Domain: calmodulin repeat homology <EF2>  
 F:101-133/Domain: calmodulin repeat homology <EF3>  
 F:137-169/Domain: calmodulin repeat homology <EF4>

Query Match 7.0%; Score 67.5; DB 2; Length 172;  
 Best Local Similarity 25.6%; Pred. No. 16+02;  
 Matches 33; Conservative 25; Mismatches 54; Indels 17; Gaps 6;

Qy 10 FLIDGSGIIPHDPRKPEFVSTWEOQKKSTLFLSMQYSEFRHPTFKFQNNPR 69  
 Db 40 FQVDSGSI---DAKELVAMRALGFEPKEKMKMISRVDRGTGKISFNDF----- 89

Qy 70 SLVKPIITOLLGTHATGIRKVRLEFNITNGARNAPKILVITD--GKFGDPLGYED 127  
 Db 90 --LAVNTQKSEKUTKEELKAFR-LPD-ODGTGKISFKNLKVAVNELGENUTDE-ELQE 144

Qy 128 VPEADREG 136  
 Db 145 MIDEADREG 153

RESULT 12  
 A64330  
 hypothetical protein MJ0240 - Methanococcus jannaschii  
 C:Species: Methanococcus jannaschii  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004  
 C:Accession: A64330  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,

; Reich, C.I.; Overbeek, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glodek, reon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Huret, M.A.  
 Science 273, 1058-1073, 1996  
 A:Authors: Kane, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese  
 A:Title: Complete genome sequence of the hyperthermophilic ciliated protozoan, Methanococcus jannaschii  
 A:Reference number: A64330; MUID:21359325; PMID:8688087  
 A:Accession: A64330  
 A:Molecule type: DNA  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Residues: 1-175 <BUL>  
 A:Cross-references: UNIPROT:Q57692; GB:U67479; GB:L77117; NID:g1590965; PIDN:AAB98225  
 A:Experimental source: strain  
 C:Genetics:  
 C:Superfamily: Thermophilic adenylate cyclase, CyaB type

Query Match 7.0%; Score 67.5; DB 2; Length 175;  
 Best Local Similarity 24.7%; Pred. No. 1.2e+02;  
 Matches 41; Conservative 20; Mismatches 64; Indels 41; Gaps 6;

Qy 33 VMEQKKSTLFLSMQYSEFRHPTFKFQNNPNSLVKPIITOLLGTHATGIRKVV 92  
 Db 16 VVEQKKLGLKFKKGFQFOIYFNGIDRDFR-----ETDEALRIDED 58

Qy 93 RELFNITNGAR-----KNAFKILVITDQKFGD---SLGYEVQVTP-----EADRE 135  
 Db 59 GIFFVTKGPKIDKISKREIEVKIEDKQRQIPKGLQFKEVPPKIRKIRIYKEDIE 118

Qy 136 GVRYVIGVGDAPFSEKSRQELNTIASKPPRHVPOVNNFEALKTI 181  
 Db 119 ASDIDVEGLGLPLELSEKISIDIN-----EKDKYLE-EMWEILKAL 157

RESULT 13  
 C71706  
 hypothetical protein RP470 - Rickettsia prowazekii  
 C:Species: Rickettsia prowazekii  
 C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
 R:Anderson, S.G.B.; Zomorodipour, A.; Anderson, J.O.; Scharitz-Ponten, T.; Alenmark  
 Nature 396, 133-140, 1998  
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
 A:Reference number: A71630; MUID:99039499; PMID:9823893  
 A:Accession: C71706  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-150 <AND>  
 A:Cross-references: UNIPROT:Q92D74; GB:A235271; GB:A235269; NID:g3868717; PIDN:CAAL  
 A:Experimental source: strain Madrid 8  
 C:Genetics:  
 C:Superfamily: Rickettsia prowazekii hypothetical protein RP470

Query Match 6.9%; Score 67; DB 2; Length 150;  
 Best Local Similarity 30.5%; Pred. No. 1e+02;  
 Matches 18; Conservative 11; Mismatches 28; Indels 2; Gaps 2;

Qy 62 FQNNPNSLVKPIITOLLGTHATGIRKVRLEFNITNGARNAPKILVITDQKFG 120  
 Db 58 IQNKSTFQSLFPTSLDTEHKEAA-RSVIKLEKVT-ANQAKYKELIILASPKMLG 114

RESULT 14  
 A96901  
 uncharacterized conserved protein, ortholog of YRKA B. subtilis CAC0009 (imported) -  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: A96901  
 R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome sequence and comparative analysis of the solvent-producing bacterium  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: A96901

Search completed: November 14, 2005, 17:38:17  
Job time : 40 secs

Result	Query	Score	Match	Length	DB	ID	Description
1	08HV27	293	30.4	79	2	08HV27	08HV27 ovis aries
2	08HV41	293	30.4	79	2	08HV41	08HV41 bos taurus
3	071V33	127.5	13.2	156	2	071V33	071V33 homo sapien
4	06AP53	89	9.2	171	2	06AP53	06AP53 desulfotale
5	063LC8	82	8.5	184	2	063LC8	063LC8 burkholderi
6	063YNA	82	8.5	184	2	063YNA	063YNA burkholderi
7	065WFS	77	8.1	153	2	065WFS	065WFS mammothia
8	060.5	80.5	8.3	162	2	0749A4	0749A4 geobacter s
9	79.5	79.5	8.2	179	2	06BGV4	06BGV4 debaryomyce
10	78.5	78.5	8.1	151	2	067PF5	067PF5 clostridium
11	78.5	78.5	8.1	166	1	1P16_CLOPE	1P16_CLOPE
12	78	78	7.7	145	2	08HV27	08HV27 ovis aries
13	77	77	7.7	145	2	08HV41	08HV41 bos taurus
14	73.5	72.5	7.6	187	2	08AVL5	08AVL5 bacillus ba
15	72.5	72.5	7.5	135	2	06LTV3	06LTV3 photobacter
16	72.5	7.5	7.5	139	2	0721N1	0721N1 leptospira
17	72.5	7.5	7.5	139	2	08FL6	08FL6 leptospira
18	72.5	7.5	7.5	148	2	06GFP9	06GFP9 staphylococ
19	72.5	7.5	7.5	168	2	08LI07	08LI07 plasmodium
20	72.5	7.5	7.5	186	1	RS7_METH	027130 methanobact
21	72	7.5	7.5	169	2	07RNB4	07RNB4 mycoplasma
22	72	7.5	7.5	170	2	07VC77	07VC77 prochloroco
23	71.5	7.4	7.4	168	2	07R941	07R941 plasmodium
24	71.5	7.4	7.4	169	2	067822	067822 aquifex aco
25	71	7.4	7.4	127	2	0712G6	0712G6 bacteriopho
26	70.5	7.3	7.3	143	2	07RNB3	07RNB3 bos taurus
27	70.5	7.3	7.3	148	2	07RNB3	07RNB3 bos taurus
28	70.5	7.3	7.3	171	2	07V4N6	07V4N6 nanorhachu
29	70.5	7.3	7.3	181	1	Y063_METJA	060375 methanococ
30	70.5	7.3	7.3	187	2	08ZER2	08ZER2 versinia pe
31	70	7.3	7.3	159	1	HBL2_GOSHI	093492 tossevpium h

[illegible]



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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 111
RP SEQUENCE FROM N.A.
RA Pronghorn Antelope, Sarikaya H., Bruckmaier R.M., Pfaffl M.W.,
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535320; CAD59475.1; --
DR HSSP; P11215; 1BHQ.
DR GO; GO:0007229; P: integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VNF_A.
DR Pfam; PF00092; VNA; 1.
DR PROSITE; PSS0234; VMA; 1.
DR Integrin.
KW INTEGRIN.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8943 MW; 504CDA584F86CBE CRC64;

Query Match
Best Local Similarity 30.4%; Score 293; DB 2; Length 79;
Matches 57; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 125 YEDVPEADREGVIRYVIGVGDAPRSEKSRQELNTASKPRDHVQVNNFEALQIQ 184
Db 1 YEDVPEADRKILIRYVIGVGDAPRSEKSRQELNTASKPRDHVQVNNFEALQIQ 60

Oy 185 LRKX 188
Db 61 LQKX 64

RESULT 3
O71V33
ID Q71V33 PRELIMINARY; PRT; 156 AA.
AC Q71V33;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DR EMBL; AJ535320; CAD59475.1; --
DR HSSP; P11215; 1BHQ.
DR GO; GO:0007229; P: integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VNF_A.
DR Pfam; PF00092; VNA; 1.
DR PRINTS; PR00453; VNFADOMAIN.
DR SMART; SM00327; VMA; 1.
DR PROSITE; PSS0234; VMA; 1.
KW Integrin.
FT NON_TER 1 1
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 17042 MW; BC7ABD63226C652B CRC64;

Query Match
Best Local Similarity 13.2%; Score 127.5; DB 2; Length 156;
Matches 38; Conservative 33; Mismatches 67; Indels 7; Gaps 3;

Oy 40 SKTLFLSMQYSEPRIFHTFKFQNNPNSRLVKPITQLLGRTHATGIRKVKRLPNI 98
Db 8 TKTVGLGVANNPRVFNPLNTYKTEKEMIVATQTSQVGGDLNTFGLGVARKAYSA 67

Oy 99 TNGARNAPKILWITGSEKFGDLYGVDPADREGVIRYVIGVGDAPRSEKSRQELNT 153
Db 68 ASGGRSATKRWVWVVDGESH-DGSKLXAVDQCWNHILNIRGLVGLYLNRALDTKUL 126
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Oy 154 ROELNTIASKPRDHVQVNNFEAL 178
Db 127 IREIKALASIPRIFFNVSDNAL 151

RESULT 4
O6AP53
ID Q6AP53 PRELIMINARY; PRT; 171 AA.
AC Q6AP53;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DR EMBL; AJ535320; CAD59475.1; --
DR HSSP; P11215; 1BHQ.
DR GO; GO:0007229; P: integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VNF_A.
DR Pfam; PF00092; VNA; 1.
DR PROSITE; PSS0234; VMA; 1.
DR Integrin.
KW INTEGRIN.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8943 MW; 504CDA584F86CBE CRC64;

Query Match
Best Local Similarity 30.4%; Score 293; DB 2; Length 79;
Matches 57; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 125 YEDVPEADREGVIRYVIGVGDAPRSEKSRQELNTASKPRDHVQVNNFEALQIQ 184
Db 1 YEDVPEADRKILIRYVIGVGDAPRSEKSRQELNTASKPRDHVQVNNFEALQIQ 60

Oy 185 LRKX 188
Db 61 LQKX 64

RESULT 3
O71V33
ID Q71V33 PRELIMINARY; PRT; 156 AA.
AC Q71V33;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DR EMBL; AJ535320; CAD59475.1; --
DR HSSP; P11215; 1BHQ.
DR GO; GO:0007229; P: integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VNF_A.
DR Pfam; PF00092; VNA; 1.
DR PRINTS; PR00453; VNFADOMAIN.
DR SMART; SM00327; VMA; 1.
DR PROSITE; PSS0234; VMA; 1.
KW Integrin.
FT NON_TER 1 1
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 17042 MW; BC7ABD63226C652B CRC64;

Query Match
Best Local Similarity 13.2%; Score 127.5; DB 2; Length 156;
Matches 38; Conservative 33; Mismatches 67; Indels 7; Gaps 3;

Oy 40 SKTLFLSMQYSEPRIFHTFKFQNNPNSRLVKPITQLLGRTHATGIRKVKRLPNI 98
Db 8 TKTVGLGVANNPRVFNPLNTYKTEKEMIVATQTSQVGGDLNTFGLGVARKAYSA 67

Oy 99 TNGARNAPKILWITGSEKFGDLYGVDPADREGVIRYVIGVGDAPRSEKSRQELNT 153
Db 68 ASGGRSATKRWVWVVDGESH-DGSKLXAVDQCWNHILNIRGLVGLYLNRALDTKUL 126
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QX	NCBI_TaxID=272560;
QY	[1]_TaxID=272560;
RP	SEQUENCE FROM N.A.
RC	STRAIN=X96243;
RX	PubMed=15377794;
RA	Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA	Akins T.C., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA	Bentley S.D., Sebathia M., Thomson N.R., Bacon N., Beacham I.R.,
RA	Crooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA	Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
RA	Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA	Keith K.E., Maddison M., Moule S., Price C., Quail M.A., Jagsels K.,
RA	Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,
RA	Songsivilai S., Stevens K., Tumapa S., Vesaatchavest M.,
RA	Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT	"Genomic plasticity of the causative agent of melioidosis,
RT	Burkholderia pseudomallei";
RD	Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
DR	EMBL; BX571965; CHN34140.1..
SR	SEQUENCE 184 AA; 20250 MW; 4C8ICEV77D6G7B82 CRG64;
QY	Query Match 8.5%; Score 82; DB 2; Length 184;
QY	Best Local Similarity 28.4%; Pred. No. 74;
QY	Matches 29; Conservative 15; Mismatches 42; Indels 16; Gaps 4;
QY	58 TFKEFQNPNPSLKVPTTOLLGTHGTATGRKVV-----VRELFNTNGAKNAFK 108
DB	59 TWKDYWFOVGARVKAMIRARKKGTAALAVCSGANVAHWEKPKRGPGTPE 118
QY	109 ILLVITDKEXEDPLGYE---DVTPEAR--EGVTRKYVTQG 145
DB	119 LLMTV--GARDGPATAYEVADIAEVDRAKRGTATHTFTQG 158
RESULT 6	
QIDYN4	
ID1	Q63YN4 PRELIMINARY; PRT; 184 AA.
AC	Q63YN4;
DC	25-OCT-2004 (TEMBLrel. 28, Created)
DT	25-OCT-2004 (TEMBLrel. 28, last sequence update)
DD	25-OCT-2004 (TEMBLrel. 28, last annotation update)
OS	Burkholderia pseudomallei
GN	OPNames=BPS0153;
GS	Burkholderia pseudomallei K96243.
OC	Bacteria; Proteobacterae; Betaproteobacteria; Burkholderiales;
CC	Burkholderiaceae; Burkholderia.
ON	NCBI_TaxID=272560;
RX	[1]
RC	SEQUENCE FROM N.A.
RC	STRAIN=X96243;
RX	PubMed=15377794;
RA	Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA	Akins T.C., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA	Bentley S.D., Sebathia M., Thomson N.R., Bacon N., Beacham I.R.,
RA	Crooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA	Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
RA	Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA	Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA	Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,
RA	Songsivilai S., Stevens K., Tumapa S., Vesaatchavest M.,
RA	Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT	"Genomic plasticity of the causative agent of melioidosis,
RT	Burkholderia pseudomallei";
RD	Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
DR	EMBL; BX571965; CHN34140.1..
SR	SEQUENCE 184 AA; 20250 MW; 59C09A77D6G7B82 CRG64;
QY	Query Match 8.5%; Score 82; DB 2; Length 184;
QY	Best Local Similarity 28.4%; Pred. No. 74;
QY	Matches 29; Conservative 15; Mismatches 42; Indels 16; Gaps 4;
QY	58 TFKEFQNPNPSLKVPTTOLLGTHGTATGRKVV-----VRELFNTNGAKNAFK 108

Db 59 TWKDYWPQYVKARVKAARIKCKTAAAVREVCSAFGNVANREWFKTPKGRPGTPE 110  
 QY 109 ILVITDGEKFGDPUGVE---DWIPEADR--EGVIRVVIUGV 145  
 Db 119 ILMTV--GARDGIPATYVADIIIAEVDRAKRGTAHYTFQGS 158  
  
 RESULT 7  
 Q5W5FS PRELIMINARY; PRT; 153 AA.  
 AC Q5W5FS  
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 DE ORFNames=MS0098;  
 GN Mannheimia succiniciproducens MBEL55E.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Mannheimia.  
 OC NCBI\_TaxID=221986;  
 RN 11\_SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MBEL55E;  
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,  
 RA Kim C.H., Jeong H., Hur C.-G., Kim J.-G.;  
 RA "The genome sequence of the capnophilic rumen bacterium Mannheimia  
 succiniciproducens";  
 RT Nat. Biotechnol. 0:0-0(2004).  
 RX EMBL: AC016927; RA05705.1; -.  
 RX NCBI: AC016927; RA05705.1; -.  
 SQ SEQUENCE 153 AA; 17160 MW; 74742F0CDDC3P78 CRC64;  
 Query Match 8.4%; Score 81; DB 2; Length 153;  
 Best Local Similarity 31.2%; Pred. No. 73;  
 Matches 34; Conservative 20; Mismatches 37; Indels 18; Gaps 7;  
  
 QY 22 DFRMKFVFSTVMEQLSKTSLFSLMOYSEFP-RHIFTFKRFQNNPRSLVLPKPTQLGG 80  
 Db 8 DTQVAKL-LQSVAAQLKARPRRIYAL--GELKKLHDFRFTKDPNG----KPMTPLA 60  
 QY 81 RHTVATGR---KVVRELFNITNGARNAKPLVIVTGGKFGDPLG 125  
 Db 61 KTLARKKRGKSLKILQDGNLAN---NTAYNIL---DDGVFSGPEVY 103  
  
 RESULT 8  
 Q749A4 PRELIMINARY; PRT; 162 AA.  
 ID Q749A4  
 AC Q749A4; 2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Ribosomal protein S5.  
 GN Name=rpS5; OrderedLocusNames=GSU2840;  
 GN Geobacter sulfurreducens.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;  
 OC Geobacteriaceae; Geobacter.  
 OC NCBI\_TaxID=35554;  
 RN 11\_SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GC-1; ATCC 51573;  
 RA PubMed=14671304; DOI=10.1126/science.1088727;  
 RA Merhe B.A., Nelson K.E., Eiseu J.A., Paulsen I.T., Nelson S.C.,  
 RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,  
 RA Madupu R., Kolonay J.F., Daugherty S.C., DeBoy R.T., Durkin A.S.,  
 RA Gwinn M.L., Brinkac J.M., Sullivan S.A., Haft D.H., Selengut J.A.,  
 RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,  
 RA Weidman J.P., Khouri H.M., Feldblyum T.V., Otterback T.R.,  
 RA von Aken B., Lovley D.R., Kaiser C.M.,  
 RA "Genome of the anaerobic bacterium Geobacter sulfurreducens: metal reduction in subsurface  
 environments";  
 RT Science 302:1967-1969(2003).  
 CC -1- SIMILARITY: Belongs to the ribosomal protein S5P family.

```

SO SEQUENCE      179 AA;    20118 MW;   5F34BA42DD342AB9 CRC64;

Query Match          8.2%; Score 79.5; DB 2; Length 179;
Best Local Similarity 23.6%; Pred. No. 1.1e-02;
Matches 38; Conservative 28; Mismatches 58; Indels . 37; Gaps ?

QY QY 37 KPTVTSMEQLKSKTTLFLMQHVSBEFFI--IHFTKFQNNP--NPRSLVKPKITOLLGRT 82
DB DB 39 IQFSNQLLSQSR---LYSVLSTSPENKLKYKENVKSIINNPSAHPDSLIIVD----- 86
OY OY 83 HTATGTGRVRELFNFMTNGAKNAFKILUVIDTG-----SKFGDLGYEDVIPEADREG 136
DB DB 87 -----VRSEVEYEDECHIPNAINIPPSSPGALOLSPREFNFUNFGFDK--PSKDKEU 135
QY QY 137 VIRVVGIGVDAFRSEKSQRLENTIAASKPPRDHVFOVNFEA 177
DB DB 136 IFYLCLAGV----RSTAASELAIDTFYGKGNGYGVSYEDMAA 172


RESULT 10
ID OCYFFS PRELIMINARY: PRT; 151 AA.
AC AC 06YFFS;
DT DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE DE Resistance protein Candidate fragment).
DE DE Eukaryotic Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC OC Campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
OX OX NCBI_TaxId=4232;
RP RP [1]
RN RN SEQUENCE FROM N.A.
RL RL PLOCIC A.M., Layden J., Keseli R.V.;
RA RA Submitted (SEP-2004) GenBank/EMBL/DDBJ databases.
DR DR PFAM: PF00931; NB-ARC;
DR DR Pfam: PF00931; NB-ARC;
FT FT NON TER 1
FT FT NON TER 151
SQ SEQUENCE 151 AA; 17071 MW; AL32AA05FC7076F1 CRC64;

Query Match          9.8%; Score 78.5; DB 2; Length 151;
Best Local Similarity 28.8%; Pred. No. 1.1e-02;
Matches 38; Conservative 21; Mismatches 46; Indels 27; Gaps 9;

QY QY 33 VMLQKKGS--KTLSLMQYSSEPIRHFTKFQNNFNPSLRVLKPITOLLGRT--HTATG 87
DB DB 1 LMSGLKKAIVEDLKMPDIV-----VKVLTGS--NTDPISLQAARYIGNLVETGG 50
OY OY 88 IR-KVYRELFINTEARNAFKILUWTDGEX-----FG-DPL--GYEDVIPHEADREGV 137
DB DB 51 AAAERLRKIIEVKSQQOK--KILVMODIWKEVELDFGLSUPNLGLKLLTFRSFNVWC 108
QY QY 138 TRVTVGDADF 149
DB DB 109 THMGVUGSIGFR 120


RESULT 11
ID YP16_CLOPE STANDARD: PRT; 166 AA.
AC AT 01-NOV-1990 (Rel. 16, Created)
AC AT 01-NOV-1990 (Rel. 16, Last sequence update)
AC AT 01-NOV-1990 (Rel. 16, Last annotation update)
DE DE Hypothetical lin_7 kDa protein (ORF6).
DE DE Clostridium perfringens.
OG OG Plasmid pJP404.
OG OG Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC OC Clostridium.
```



```
DB 20 PRKSKFVNOAYMDU-----TSFHYVYMKR-KIH-----KIMMNYN----- 56
QY 83 HTATGRTVRELENTINGAKAKAKKI 109
DB 57 -----NEK-IQSMNLINKEKENAYKI 78

RESULT 14
OSKATS
ID OSKATS PRELIMINARY: PRT: 187 AA.
AC OSKATS;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 24, Last annotation update)
DE BH2201
GN OrderedLocusNames=BH2201;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RA MEDLINE=20512562; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RX Takami H., Nakasone K., Tokaki Y., Mieno G., Sasaki K., Masui N.,
RA Fujita K., Kame C., Nakamura Y., Ogasawara N., Aihara S.,
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AF001514; BAB05920.1; -.
DR PIR; A83925; A83925.
DR InterPro; IPR007353; DUF421.
DR Pfam; PF04239; DUF421; 1.
KW Complete proteome.
SQ SEQUENCE 187 AA; 21751 MW; 33C0341D633C5836 CRC64;

Query Match 7.6%; Score 73.5; DB 2; Length 187;
Best Local Similarity 22.6%; Pred. No. 3.7e+02;
Matches 38; Conservative 32; Mismatches 59; Indels 39; Gaps 8;

OY 12 IDGSGIIPHDFRMRKEFVSTMEQKKSKTLFSLMOYSEFRIH--FTFKFQNNPNR 69
DB 47 LDGTPTLLIQDGKLE-----HNKKEN--FSIDMFQALREKEIFDMQVE----- 91
OY 70 SILVKPTTOLLGRTHATGIRK-----VRELFTNGAKAKNAFKILVITDQKPGDPLG 124
DB 92 -----TALTDGTGVLVKRPYLPVTRKDLNIPVAKHRPTELI---DOENVKENLL 142
OY 125 YEDVIPADREGVIRYVGVGDAPRS---EKSROELMTIASKEPRDHV 169
DB 143 ENDLSEWMLKQIBILRGYGIQDVYFVAVLDKSGRLVLDTY-----RDHL 185

RESULT 15
QELTV3
ID QELTV3 PRELIMINARY: PRT: 135 AA.
AC QELTV3;
DT 05-JUN-2004 (TEMBLrel. 27, Created)
DT 05-JUN-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TEMBLrel. 27, Last annotation update)
DE Hypothetical protein
GN OrderedLocusNames=PBPA0859;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cecchi A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valli G.
RT "Genome analysis of Photobacterium profundum reveals the complexity of
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RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RX EMBL; CX378695; DDBJ; EMBL; F019999.1;
KW Accession: Proteome; Hypothetical protein.
SQ SEQUENCE 135 AA; 14724 MW; 986784595286B333 CRC64;

Query Match 7.5%; Score 72.5; DB 2; Length 135;
Best Local Similarity 25.2%; Pred. No. 3.1e+02;
Matches 27; Conservative 19; Mismatches 32; Indels 29; Gaps 4;

OY 27 KSFVSTVMEQLKSKTLF-----SLMOYS-REPRIHTPKFQNNPN 67
DB 37 KQSVTSLGLLPSEETIIFGTSDEGNSRELVSALLEYSAEYSAEYKIAFTIKERLDOGA 96
OY 68 PSLVWKPTTOLLGRTHATGIRKVVRELFTNGAKAKNAFKILVIT 114
DB 97 WRTIISPV-----LSTGLNEPTS--FVSTNDASKEHVKLOVEVT 133

Search completed: November 14, 2005, 17:37:33
Job time : 175 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2005, 17:26:24 ; Search time 43 Seconds  
(without alignments)  
326.373 Million cell updates/sec

Title: US-09-758-493-1\_COPY\_1\_188

Perfect score: 965  
Sequence: 1 CPODSDIADLDGSGIIP.....VQVNNFEALQINQLREK 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 387217

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents: AA.\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/5C\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/5D\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/5E\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/5F\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	960	99.5	187	2	US-08-177-109A-61
2	960	99.5	187	2	US-08-687-706-61
3	534	55.3	187	2	US-08-177-109A-62
4	534	55.3	187	2	US-08-687-706-62
5	534	55.3	187	5	PCT-US96-01314-60
6	286.5	29.7	184	3	US-08-974-899-7
7	286.5	29.7	184	4	US-09-795-789-7
8	281.3	28.2	184	3	US-08-974-899-8
9	281.3	28.2	184	3	US-08-974-899-8
10	266	27.6	181	5	US-08-795-799-8
11	171	17.7	33	2	US-08-476-062A-61
12	171	17.7	33	2	PCT-US96-01314-50
13	146	15.1	28	2	US-08-476-062A-10
14	146	15.1	28	5	PCT-US96-01314-10
15	129	13.4	25	2	US-08-476-062A-8
16	129	13.4	25	5	PCT-US96-01314-68
17	126	13.1	29	5	PCT-US96-01314-69
18	125	13.0	24	5	PCT-US96-01314-69
19	117	12.1	22	2	US-08-476-062A-12
20	117	12.1	22	5	PCT-US96-01314-12
21	113	11.7	22	5	PCT-US96-01314-16
22	113	11.7	22	5	PCT-US96-01314-22
23	113	11.7	22	5	PCT-US96-01314-22
24	112	11.6	21	2	US-08-476-062A-7
25	112	11.6	21	5	PCT-US96-01314-7
26	111	11.5	20	5	PCT-US96-01314-65
27	110	11.4	20	2	US-08-476-062A-17

Sequence 17, Appl  
Sequence 70, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 62, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 43, Appl  
Sequence 73, Appl  
Sequence 6, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 56, Appl  
Sequence 64, Appl  
Sequence 1, Appl  
Sequence 71, Appl

## ALIGNMENTS

RESULT 1  
US-08-177-109A-61  
Sequence 61, Application US/08177109A  
Patent No. 682615  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Ogleby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fatma L. Babst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
STATE: Atlanta  
COUNTRY: US  
ZIP: 30309-1450  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/177,109A  
FILING DATE: 01-JAN-1994  
CLASSIFICATION: C14  
ATTORNEY/AGENT INFORMATION:  
NAME: Babst, Fatma L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: Protein  
HYPOTHETICAL: NO  
US-08-177-109A-61

Query Match 99.5%; Score 960; DB 2; Length 187;  
Best Local Similarity 100.0%; Pred. No. 3.4e-96;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CPODSDIADLDGSGIIPHDPRKMFVSTVMQKSKTLPFLSMQYSEPRHPTFK 60  
DB 1 CPODSDIADLDGSGIIPHDPRKMFVSTVMQKSKTLPFLSMQYSEPRHPTFK 60  
QY '61 EFQNNPNSRLVKEITQLGCHTATATGIRKVRRELFNITNGARKAPKILVITDGEKFG 120

Db 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Oy 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180  
Db 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180  
Oy 181 IONQLRE 187  
Db 181 IONQLRE 187

RESULT 2  
US-08-687-706-61  
Sequence 61, Application US/08687706  
Patent No. 5869615  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/687,706  
FILING DATE: 26-JUL-1996  
CLASSIFICATION: 514  
PRIORITY INFORMATION:  
PRIORITY NUMBER: US 08/177,109  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8795  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQUENCING:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO

US-08-687-706-61

Query Match 99.5%; Score 960; DB 2; Length 187;  
Best Local Similarity 100.0%; Pred. No. 3.4e-96;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFEFVSTWMLQKSKTFLSLMOYSEEFRIHFTFK 60  
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFEFVSTWMLQKSKTFLSLMOYSEEFRIHFTFK 60  
Oy 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Db 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Oy 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180  
Db 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180

Query Match 99.5%; Score 960; DB 2; Length 187;  
Best Local Similarity 100.0%; Pred. No. 3.4e-96;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFEFVSTWMLQKSKTFLSLMOYSEEFRIHFTFK 60  
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFEFVSTWMLQKSKTFLSLMOYSEEFRIHFTFK 60  
Oy 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Db 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Oy 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180  
Db 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180

Oy 181 IONQLRE 187  
Db 181 IONQLRE 187  
RESULT 3  
US-08-177-109A-62  
Sequence 62, Application US/08177109A  
Patent No. 5869615  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/177,109A  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8795  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQUENCING:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO

US-08-177-109A-62

Query Match 55.3%; Score 534; DB 2; Length 187;  
Best Local Similarity 55.6%; Pred. No. 5.4e-50;  
Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;  
Oy 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFEFVSTWMLQKSKTFLSLMOYSEEFRIHFTFK 60  
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFEFVSTWMLQKSKTFLSLMOYSEEFRIHFTFK 60  
Oy 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Db 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Oy 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180  
Db 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180

US-08-177-109A-62

Query Match 55.3%; Score 534; DB 2; Length 187;  
Best Local Similarity 55.6%; Pred. No. 5.4e-50;  
Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;  
Oy 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFEFVSTWMLQKSKTFLSLMOYSEEFRIHFTFK 60  
Db 1 CPQEDSDIAFLIDGSGSIIPHDPRMKFEFVSTWMLQKSKTFLSLMOYSEEFRIHFTFK 60  
Oy 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Db 61 EFQNNPNSLVKPTQLGRTHTATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120  
Oy 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180  
Db 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDHVFOVNNFALKT 180

US-08-687-706-62  
Sequence 62, Application US/08687706  
Patent No. 5928892  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby





```

; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; INVENTOR: Lee, Wendy M.
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-974-899-7
;
; Query Match 29.7%; Score 286.5; DB 3; Length 184;
; Best Local Similarity 33.5%; Pred. No. 3.6e-23;
; Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
;
; Oy 7 DIATLDGSGSIIPHDFRMKEFVSTWOLKSKTFLSLMOVSEPRHFTFKFQNNP 66
; Db 5 DLVFLDGSMSLQDFEKFILDMKDVKKLSNTSYQFAAVQFSTSYKTFDFSDYVKRK 64
;
; Oy 67 NPRLSVKPTITGLGTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFDPLGYE 126
; Db 65 DPDLALKHVMHLLNTFGAINVYATVFRFELGARDPAKVKLIITDGE--ATDSGNI 122
;
; Oy 127 DVTPDAREGVIRVIGDGFSEKROELNTASKPRDHVQFVNNFEALKTIONQLR 186
; Db 123 DAAKO-----IIRVIGIRGHQFKTSQETLHKFASKPASEFVKILDTPEKILDTFELQ 177
;
; Oy 187 EK 188
; Db 178 KK 179
;
; RESULT 7
; US-09-795-798-7
; Sequence 7, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; INVENTOR: Presta, Leonard G.
; CORRESPONDENCE ADDRESS:
; APPLICANT: Presta, Leonard G.
; ADDRESS:
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1

```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-09-795-798-7
;
; Query Match 29.7%; Score 286.5; DB 4; Length 184;
; Best Local Similarity 33.5%; Pred. No. 3.6e-23;
; Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
;
; Oy 7 DIATLDGSGSIIPHDFRMKEFVSTWOLKSKTFLSLMOVSEPRHFTFKFQNNP 66
; Db 5 DLVFLDGSMSLQDFEKFILDMKDVKKLSNTSYQFAAVQFSTSYKTFDFSDYVKRK 64
;
; Oy 67 NPRLSVKPTITGLGTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFDPLGYE 126
; Db 65 DPDLALKHVMHLLNTFGAINVYATVFRFELGARDPAKVKLIITDGE--ATDSGNI 122
;
; Oy 127 DVTPDAREGVIRVIGDGFSEKROELNTASKPRDHVQFVNNFEALKTIONQLR 186
; Db 123 DAAKO-----IIRVIGIRGHQFKTSQETLHKFASKPASEFVKILDTPEKILDTFELQ 177
;
; Oy 187 EK 188
; Db 178 KK 179
;
; RESULT 8
; US-08-974-899-8
; Sequence 8, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; INVENTOR: Presta, Leonard G.
; CORRESPONDENCE ADDRESS:
; APPLICANT: Presta, Leonard G.
; ADDRESS:
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-974-899-8

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Query Match      29.2%; Score 281.5; DB 3; Length 184;
Best Local Similarity 33.0%; Pred. No. 1.3e-22;
Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAFLDGSGLIPHDPRMKEFVTVMEQLKSKTFLSLMOYSEFEFRIHFTKFPQNP 66
Db 5 DLFLFDGMSLQDFQKILDPKMDVKKLSNTSYQFAAVQSTYKTEFDFSDYVQK 64

Qy 67 NPSLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGYE 126
Db 65 DPDLLENVGMELLNTFGALINYVATEVFEELGARDPKATKVLIIITDGS--ATDSGNI 122

Qy 127 DVLPADREGVIRVYGVGDADFSEKSRQELNTIASKPRDHYFOVNNFEALKTIONLR 186
Db 123 DAAKD-----IIRVIIGIKGHFOTKESQETLHKFASKPASEFVKILDTFEKLDPTELQ 177

Qy 187 EK 188
Db 178 KK 179

RESULT 9
; Sequence 9, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-FEB-2001
; PRIORITY: 6703018 (Unknown)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-795-798-8

Query Match      29.2%; Score 281.5; DB 4; Length 184;
Best Local Similarity 33.0%; Pred. No. 1.3e-22;
Matches 60; Conservative 46; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAFLDGSGLIPHDPRMKEFVTVMEQLKSKTFLSLMOYSEFEFRIHFTKFPQNP 66
Db 5 DLFLFDGMSLQDFQKILDPKMDVKKLSNTSYQFAAVQSTYKTEFDFSDYVQK 64

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Qy 67 NPSLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGYE 126
Db 65 DPDLLENVGMELLNTFGALINYVATEVFEELGARDPKATKVLIIITDGS--ATDSGNI 122

Qy 127 DVLPADREGVIRVYGVGDADFSEKSRQELNTIASKPRDHYFOVNNFEALKTIONLR 186
Db 123 DAAKD-----IIRVIIGIKGHFOTKESQETLHKFASKPASEFVKILDTFEKLDPTELQ 177

Qy 187 EK 188
Db 178 KK 179

RESULT 10
; Sequence 61, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Athaout
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 825 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 of 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PC/TUS96/01314
; FILING DATE: 08-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-01314-61

Query Match      27.6%; Score 266; DB 5; Length 181;
Best Local Similarity 33.0%; Pred. No. 6e-21;
Matches 60; Conservative 46; Mismatches 68; Indels 8; Gaps 3;

Qy 1 CPQSDSIAPLIDGSGSLIPHDPRMKEFVTVMEQLKSKTFLSLMOYSEFEFRIHFTK 60
Db 1 CLKGNVDLVFLFDGMSLQDFQKILDPKMDVKKLSNTSYQFAAVQSTYKTEFDFS 60

Qy 61 BFOVNPNSISLVKPIITOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 61 DYVKKDDPDLLENVGMELLNTFGALINYVATEVFEELGARDPKATKVLIIITDGS--A 118

Qy 121 DPLGYDVIPEADREGVIRVYGVGDADFSEKSRQELNTIASKPRDHYFOVNNFEALK 179
Db 119 TDSGNDAKD-----IIRVIIGIKGHFOTKESQETLHKFASKPASEFVKILDTFEKLK 173

Qy 180 TI 181

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DB 174 DL 175

RESULT 11  
US-08-476-062A-50  
Sequence 30, Application US/08476062A  
Patent No. 5877275  
GENERAL INFORMATION:  
APPLICANT: Arnaout, M. Amin  
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY  
NUMBER OF SEQUENCES: 53  
RESPONSES WITH BETA2 INTEGRINS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,062A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/216,081  
FILING DATE: 21-MAR-1994  
APPLICATION NUMBER: 07/637,830  
FILING DATE: 04-JAN-1991  
APPLICATION NUMBER: 07/539,842  
FILING DATE: 18-JUN-1990  
APPLICATION NUMBER: 07/212,573  
FILING DATE: 28-JUN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00786/068003  
TELEPHONE: (617) 542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-476-062A-50  
Query Match 17.7%; Score 171; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 NAFKILVITDGEKGPLGVEDVIEADREGV 137  
DB 1 NAFKILVITDGEKGPLGVEDVIEADREGV 33

RESULT 12  
PCT-US96-01314-50  
Sequence 50, Application PC/TUS9601114  
Patent No. 5877275  
GENERAL INFORMATION:  
APPLICANT: M. Amin Arnaout  
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN  
NUMBER OF SEQUENCES: 78  
RESPONSES WITH BETA2 INTEGRINS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,062A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/216,081  
FILING DATE: 21-MAR-1994  
APPLICATION NUMBER: 07/637,830  
FILING DATE: 04-JAN-1991  
APPLICATION NUMBER: 07/539,842  
FILING DATE: 18-JUN-1990  
APPLICATION NUMBER: 07/212,573  
FILING DATE: 28-JUN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00786/068003  
TELEPHONE: (617) 542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-476-062A-50  
Query Match 17.7%; Score 171; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 NAFKILVITDGEKGPLGVEDVIEADREGV 137  
DB 1 NAFKILVITDGEKGPLGVEDVIEADREGV 33

RESULT 13  
US-08-476-062A-10  
Sequence 10, Application US/08476062A  
Patent No. 5877275  
GENERAL INFORMATION:  
APPLICANT: Arnaout, M. Amin  
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY  
NUMBER OF SEQUENCES: 53  
RESPONSES WITH BETA2 INTEGRINS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,062A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/216,081  
FILING DATE: 21-MAR-1994  
APPLICATION NUMBER: 07/637,830  
FILING DATE: 04-JAN-1991  
APPLICATION NUMBER: 07/539,842  
FILING DATE: 18-JUN-1990  
APPLICATION NUMBER: 07/212,573  
FILING DATE: 28-JUN-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00786/068003  
TELEPHONE: (617) 542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-476-062A-10  
Query Match 17.7%; Score 171; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 NAFKILVITDGEKGPLGVEDVIEADREGV 137  
DB 1 NAFKILVITDGEKGPLGVEDVIEADREGV 33

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; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-476-062A-10

Query Match 15.1%; Score 146; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 FKILVITDGEKFGDPLGYEDVPEADR 134
Db 1 FKILVITDGEKFGDPLGYEDVPEADR 28

RESULT 14
PCT-US96-01314-10
; Sequence 10, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaut
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US96-01314-10

Query Match 15.1%; Score 146; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 FKILVITDGEKFGDPLGYEDVPEADR 134

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Db 1 FKILVITDGEKFGDPLGYEDVPEADR 28

RESULT 15
US-08-476-062A-8
; Sequence 8, Application US/08476062A
; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Arnaut, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,081
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 24-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-476-062A-8

Query Match 13.4%; Score 129; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 PNPRLSVITDGLGRTHTATGIRK 90
Db 1 PNPRLSVITDGLGRTHTATGIRK 25

Search completed: November 14, 2005, 17:39:04
Job time : 44 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2005, 17:37:39 ; Search time 164 Seconds  
(Without alignments)  
479.640 Million cell updates/sec

Title: US-09-758-493-1\_COPY\_1\_188

Perfect score: 965  
Sequence: 1 CPEQSDIAFLDGGSGIIP.....VFQVNFALNTQNLQREK 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1137175

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	939	97.3	184	15	US-10-346-863-17	Sequence 17, Appl
2	939	97.3	187	15	US-10-346-863-37	Sequence 37, Appl
3	939	97.3	187	16	US-10-615-515-9	Sequence 9, Appl
4	534	55.3	187	20	US-11-000-473-59	Sequence 59, Appl
5	333.5	34.6	176	10	US-09-976-782-38	Sequence 38, Appl
6	286.5	29.7	182	15	US-10-346-863-33	Sequence 33, Appl
7	286.5	29.7	183	15	US-10-346-863-20	Sequence 20, Appl
8	286.5	29.7	183	15	US-10-346-863-41	Sequence 41, Appl
9	286.5	29.7	183	16	US-10-615-515-7	Sequence 7, Appl
10	286.5	29.7	184	15	US-10-346-863-17	Sequence 17, Appl
11	286.5	29.7	184	10	US-09-795-798-7	Sequence 7, Appl

12	286.5	29.7	184	11	US-09-758-493-4	Sequence 4, Appl
13	286.5	29.7	184	14	US-10-474-429-2033	Sequence 2033, Appl
14	286.5	29.7	184	18	US-10-727-737-7	Sequence 7, Appl
15	286.5	29.7	184	18	US-10-727-737-7	Sequence 35, Appl
16	282.5	29.3	182	15	US-10-346-863-35	Sequence 35, Appl
17	282.5	29.3	182	15	US-10-346-863-36	Sequence 36, Appl
18	282.5	29.3	188	15	US-10-346-863-56	Sequence 56, Appl
19	281.5	29.2	184	10	US-09-795-798-8	Sequence 8, Appl
20	281.5	29.2	184	18	US-10-727-737-8	Sequence 8, Appl
21	266	27.6	181	20	US-11-000-473-60	Sequence 60, Appl
22	233	24.1	180	15	US-10-346-863-40	Sequence 40, Appl
23	233	23.9	178	9	US-09-801-76A-4	Sequence 4, Appl
24	207.1	21.5	172	15	US-10-609-378A-29	Sequence 29, Appl
25	207.1	21.5	172	15	US-10-609-378A-29	Sequence 76, Appl
26	196.5	20.4	185	16	US-10-699-035A-28	Sequence 28, Appl
27	192.5	19.9	178	15	US-10-346-863-43	Sequence 43, Appl
28	192.5	19.9	180	15	US-10-346-863-31	Sequence 31, Appl
29	192.5	19.9	180	20	US-11-047-278-3	Sequence 3, Appl
30	190.5	19.7	180	15	US-10-080-334-130	Sequence 130, Appl
31	184	19.1	182	16	US-10-699-035A-24	Sequence 24, Appl
32	183.5	19.0	176	15	US-10-699-035A-81	Sequence 81, Appl
33	179.5	18.5	150	15	US-10-346-863-30	Sequence 30, Appl
34	177.5	18.3	182	16	US-10-699-035A-22	Sequence 22, Appl
35	174.5	17.7	183	20	US-11-000-473-56	Sequence 50, Appl
36	171	17.7	177	17	US-10-087-192-1209	Sequence 1209, Appl
37	171	17.7	116	13	US-10-087-192-1209	Sequence 27, Appl
38	165.5	17.2	184	16	US-10-699-035A-27	Sequence 29, Appl
39	164.5	17.0	185	16	US-10-699-035A-29	Sequence 8, Appl
40	162.5	16.8	180	16	US-10-699-035A-8	Sequence 31, Appl
41	162.5	16.8	181	16	US-10-699-035A-31	Sequence 2, Appl
42	160.5	16.6	180	16	US-10-699-035A-2	Sequence 3, Appl
43	155.5	16.1	160	9	US-09-801-736A-3	Sequence 3310, A
44	155.5	16.1	171	9	US-09-864-761-47637	Sequence 47637, A
45	155.5	16.1	172	9	US-09-864-761-47637	

ALIGNMENTS

RESULT 1  
US-10-346-863-17  
; Sequence 17, Application US/10346863  
; Publication No. US20040038325A1  
; GENERAL INFORMATION:  
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN  
; APPLICANT: GUTTERIDGE, ALEX  
; TITLE OF INVENTION: ADHESION MOLECULES  
; CURRENT APPLICATION NUMBER: US/10/346, 863  
; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: PCT/GB01/03318  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: GB 0018126.3  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: GB 0025447.4  
; PRIOR FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 184  
; LENGTH: 184  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-10-346-863-17

Query Match 97.3%; Score 939; DB 15; Length 184;  
Best Local Similarity 100.0%; Prad. No. 7.3e-92;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 DSDIAFLDGGSGIIPHDPRFMKGVSTVMEQKSKTLPFLSLMOYSEPRHHTKPEFON 60

Qy 65 NPNSRLVPEITOLLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 124  
Db 61 NPNSRLVPEITOLLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 120  
Qy 125 YEDVIPADREGVIRVVGCDAFRSEKSEQLNTIASKPRDRHVQVNNFEALKTIONQ 184  
Db 121 YEDVIPADREGVIRVVGCDAFRSEKSEQLNTIASKPRDRHVQVNNFEALKTIONQ 180  
Qy 185 LREK 188  
Db 181 LREK 184

## RESULT 2

US-10-346-863-37  
; Sequence 37, Application US/10346863  
; Publication No. US20040038325A1  
; GENERAL INFORMATION:  
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN  
; APPLICANT: FAGAN, RICHARD JOSEPH  
; APPLICANT: GUTTERIDGE, ALEX  
; TITLE OF INVENTION: ADHESION MOLECULES  
; FILE REFERENCE: 674575-2001  
; CURRENT APPLICATION NUMBER: US/10/346,863  
; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: PCT/G801/03118  
; PRIOR FILING DATE: 2003-07-24  
; PRIOR APPLICATION NUMBER: GB 0018126.3  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: GB 0025447.4  
; PRIOR FILING DATE: 2005-10-17  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-346-863-37

Query Match 97.3%; Score 919; DB 15; Length 187;  
Best Local Similarity 100.0%; Pred. No. 7.5e-92;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 DSDIAPLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTKEFON 64  
Db 1 DSDIAPLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTKEFON 60  
Qy 65 NPNSRLVPEITOLLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 124  
Db 61 NPNSRLVPEITOLLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 120  
Qy 125 YEDVIPADREGVIRVVGCDAFRSEKSEQLNTIASKPRDRHVQVNNFEALKTIONQ 184  
Db 121 YEDVIPADREGVIRVVGCDAFRSEKSEQLNTIASKPRDRHVQVNNFEALKTIONQ 180  
Qy 185 LREK 188  
Db 181 LREK 184

## RESULT 3

US-10-615-515-9  
; Sequence 9, Application US/10615515  
; Publication No. US20040132974A1  
; GENERAL INFORMATION:  
; APPLICANT: FAGAN, RICHARD, JOSEPH  
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN  
; APPLICANT: GUTTERIDGE, ALEX  
; TITLE OF INVENTION: ADHESION MOLECULES  
; FILE REFERENCE: 674575-2004  
; CURRENT APPLICATION NUMBER: US/10/615,515  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: PCT/G802/00107

; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: GB 0100750.9  
; PRIOR FILING DATE: 2001-01-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 9  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-615-515-9

Query Match 97.3%; Score 939; DB 16; Length 187;  
Best Local Similarity 100.0%; Pred. No. 7.5e-92;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 DSDIAPLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTKEFON 64  
Db 1 DSDIAPLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTKEFON 60  
Qy 65 NPNSRLVPEITOLLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 124  
Db 61 NPNSRLVPEITOLLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFGDPLG 120  
Qy 125 YEDVIPADREGVIRVVGCDAFRSEKSEQLNTIASKPRDRHVQVNNFEALKTIONQ 184  
Db 121 YEDVIPADREGVIRVVGCDAFRSEKSEQLNTIASKPRDRHVQVNNFEALKTIONQ 180  
Qy 185 LREK 188  
Db 181 LREK 184

## RESULT 4

US-11-000-473-59  
; Sequence 59, Application US/11000473  
; Publication No. US2005027256A1  
; GENERAL INFORMATION:  
; APPLICANT: ARMOUR, M. Armin  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS  
; FILE REFERENCE: 00786-267002  
; CURRENT APPLICATION NUMBER: US/11/000,473  
; CURRENT FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: US/09/592,617  
; PRIOR FILING DATE: 2000-06-13  
; PRIOR APPLICATION NUMBER: US 08/380,167  
; PRIOR FILING DATE: 1999-01-30  
; PRIOR APPLICATION NUMBER: US 08/216,081  
; PRIOR FILING DATE: 1994-02-21  
; PRIOR APPLICATION NUMBER: US 07/637,830  
; PRIOR FILING DATE: 1991-01-04  
; PRIOR APPLICATION NUMBER: US 07/539,842  
; PRIOR FILING DATE: 1990-06-18  
; PRIOR APPLICATION NUMBER: US 07/212,573  
; PRIOR FILING DATE: 1988-06-28  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 187  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-000-473-59

Query Match 55.3%; Score 534; DB 20; Length 187;  
Best Local Similarity 55.6%; Pred. No. 1.5e-48;  
Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;  
Qy 1 CPQSDSIAPLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTKE 60  
Db 1 CPQSDSIAPLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTILFSLMOYSEEFRIHFTKE 60  
Qy 61 EFOONNPRLVPEITOLLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFG 120  
Db 61 EFOONNPRLVPEITOLLGRTHATGIRKVVRELFNTNGAKNAFKILVITDGEKFG 120

Qy 121 DPLGVDPVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPDRHVFQVNNFPAKLT 180  
Db 121 DSLQKDVIPMAADAGIIRYALVIGLAFQNRNSWKELNDIASKRSQEHFKVDFDLKD 180  
Qy 181 IQNQLRE 187  
Db 181 IQNQLKE 187  
RESULT 5  
US-09-976-782-38  
; Sequence 38, Application US/09976782  
; Publication No. US20010190715A1  
; GENERAL INFORMATION:  
; APPLICANT: Grosse et al  
; TITLE OF INVENTION: NO. US20030190715a1e1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-157  
; CURRENT APPLICATION NUMBER: US/09/976.782  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240.113  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240.662  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240.732  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/240.625  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/240.703  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/241.190  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/240.637  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/240.669  
; PRIOR FILING DATE: 2000-10-16  
; PRIOR APPLICATION NUMBER: 60/262.455  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: 60/240.648  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence:Consensus  
; OTHER INFORMATION: sequence  
US-09-976-782-38  
Query Match 34.6%; Score 333.5; DB 10; Length 176;  
Best Local Similarity 43.4%; Pred. No. 3.6e-27;  
Matches 79; Conservative 29; Mismatches 65; Indels 9; Gaps 4;  
Qy 7 DIAPLDGSGSIIPHDPRRMKEFVSTVMEQLKSKTKLFSLMQYSEBRIHFTKFPQN 64  
Db 1 DIVLLDGGSGIQNFQVDFVVERVLDIGDKRVGLVQISDVRTEFLANDIQN 60  
Qy 65 NENPRESLVKPTQL-LGSHTHATGIRKVVRLFNITNGARKNAKPLVITDGSKFGDPL 123  
Db 61 KDEVLQALKIYYGGGCTGTGALQVYVRLFTASGSGREGAPKVLVLTDGSCDDPI 120  
Qy 124 GYEDVPEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPDRHVFQVNNFPAKLTQN 183  
Db 121 --RDVLNKLKAGVNVFAIGVGNADNVE---ELREIASKPDQEHVPKVSDFEALDTIOR 174  
Qy 184 QL 185  
Db 175 LL 176

RESULT 6

US-10-346-863-33  
; Sequence 33, Application US/10346863  
; Publication No. US20040038325A1  
; GENERAL INFORMATION:  
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN  
; APPLICANT: FAGAN, RICHARD JOSEPH  
; APPLICANT: GUTTERIDGE, ALEX  
; TITLE OF INVENTION: ADHESION MOLECULES  
; FILE REFERENCE: 674575-2001  
; CURRENT APPLICATION NUMBER: US/10/346.863  
; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: PCT/GB01/03318  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: GB 0018126.3  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: GB 0025447.4  
; PRIOR FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-346-863-33  
Query Match 29.7%; Score 286.5; DB 15; Length 182;  
Best Local Similarity 33.5%; Pred. No. 2.6e-24;  
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;  
Qy 7 DIAPLDGSGSIIPHDPRRMKEFVSTVMEQLKSKTKLFSLMQYSEBRIHFTKFPQN 66  
Db 4 DLVFLDGGSGSLQDFQKILDPKQVNMKLSNTSYQFAAVQFSTSYKTFDFSDYVKRK 63  
Qy 67 NPSRLVKTPLLQTHGTATGIRKVVRLFNITNGARKNAKPLVITDGSKFGDPLGYE 126  
Db 64 DEDALKHVMILLTNTFGALNTVATEVPEELGAPDPATKVLIIITDGR--ATDSGTI 121  
Qy 127 DYTEADREGVIRYVIGVDAPFSEKSRQELNTIASKPPDRHVFQVNNFPAKLTQNOLR 186  
Db 122 DAAXD----LIRYIIGIKRFPQTKSQETLHKFASKPASEFVKILDTTEKLNQLFTQL 176  
Qy 187 EK 188  
Db 177 KK 178  
RESULT 7  
US-10-346-863-20  
; Sequence 20, Application US/10346863  
; Publication No. US20040038325A1  
; GENERAL INFORMATION:  
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN  
; APPLICANT: FAGAN, RICHARD JOSEPH  
; APPLICANT: GUTTERIDGE, ALEX  
; TITLE OF INVENTION: ADHESION MOLECULES  
; FILE REFERENCE: 674575-2001  
; CURRENT APPLICATION NUMBER: US/10/346.863  
; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: PCT/GB01/03318  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: GB 0018126.3  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: GB 0025447.4  
; PRIOR FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-346-863-20  
Query Match 29.7%; Score 286.5; DB 15; Length 183;

Best Local Similarity 33.5%; Pred. No. 4e-22;  
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;  
Qy 7 DIAPLIDGSGSIIPHDFRMKEFVSTWQKLSKTLPSLMQYSEPRHFTFKFQNP 66  
Db 4 DLVFLFGSGNSLQDFEKFILDFMKDVKKLSNTSYQFAVQSTSYKTEFDSFYVKR 63  
Qy 67 NPSRLVKPITOLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFDPLGYE 126  
Db 64 DPDALLKHVGHMLLNTFGAINVATEVFRELGPATKVLIIITDGE--ATDSGNI 121  
Qy 127 DVIPADREGVIRYVIGVDAPFSEKSGRELNTIASKPRDHVFNFNFEALKTIONOLR 186  
Db 122 DAADK-----IIRYIGIGKHGFTQESQETLHKFASKPASEFVKILDTPEKLDLPTELQ 176  
Qy 187 EK 188  
Db 177 KK 178

RESULT 8  
US-10-346-863-41  
; Sequence 41, Application US/10346863  
; Publication No. US20040039325A1  
; GENERAL INFORMATION:  
; APPLICANT: PAGAN, CHRISTOPHER BENJAMIN  
; APPLICANT: PAGAN, RICHARD JOSEPH  
; APPLICANT: GUTTERIDGE, ALEX  
; TITLE OF INVENTION: ADHESION MOLECULES  
; FILE REFERENCE: 674575-2001  
; CURRENT APPLICATION NUMBER: US/10/346.863  
; PRIOR FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: PCT/GB01/03318  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: GB 0018126.3  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: GB 025447.4  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-346-863-41

Query Match 29.7%; Score 286.5; DB 15; Length 183;  
Best Local Similarity 33.5%; Pred. No. 4e-22;  
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;  
Qy 7 DIAPLIDGSGSIIPHDFRMKEFVSTWQKLSKTLPSLMQYSEPRHFTFKFQNP 66  
Db 4 DLVFLFGSGNSLQDFEKFILDFMKDVKKLSNTSYQFAVQSTSYKTEFDSFYVKR 63  
Qy 67 NPSRLVKPITOLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFDPLGYE 126  
Db 64 DPDALLKHVGHMLLNTFGAINVATEVFRELGPATKVLIIITDGE--ATDSGNI 121  
Qy 127 DVIPADREGVIRYVIGVDAPFSEKSGRELNTIASKPRDHVFNFNFEALKTIONOLR 186  
Db 122 DAADK-----IIRYIGIGKHGFTQESQETLHKFASKPASEFVKILDTPEKLDLPTELQ 176  
Qy 187 EK 188  
Db 177 KK 178

RESULT 9  
US-10-615-515-7  
; Sequence 7, Application US/10615515  
; Publication No. US20040132974A1  
; GENERAL INFORMATION:  
; APPLICANT: PAGAN, RICHARD, JOSEPH

; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN  
; APPLICANT: GUTTERIDGE, ALEX  
; TITLE OF INVENTION: ADHESION MOLECULES  
; FILE REFERENCE: 674575-2004 US/10/615.515  
; CURRENT APPLICATION NUMBER: US/10/615.515  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: PCT/GB02/00107  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: GB 0100750.9  
; PRIOR FILING DATE: 2001-01-11  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 7  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-615-515-7

Query Match 29.7%; Score 286.5; DB 16; Length 183;  
Best Local Similarity 33.5%; Pred. No. 4e-22;  
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;  
Qy 7 DIAPLIDGSGSIIPHDFRMKEFVSTWQKLSKTLPSLMQYSEPRHFTFKFQNP 66  
Db 4 DLVFLFGSGNSLQDFEKFILDFMKDVKKLSNTSYQFAVQSTSYKTEFDSFYVKR 63  
Qy 67 NPSRLVKPITOLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFDPLGYE 126  
Db 64 DPDALLKHVGHMLLNTFGAINVATEVFRELGPATKVLIIITDGE--ATDSGNI 121  
Qy 127 DVIPADREGVIRYVIGVDAPFSEKSGRELNTIASKPRDHVFNFNFEALKTIONOLR 186  
Db 122 DAADK-----IIRYIGIGKHGFTQESQETLHKFASKPASEFVKILDTPEKLDLPTELQ 176  
Qy 187 EK 188  
Db 177 KK 178

RESULT 10  
US-09-805-354-4  
; Sequence 4, Application US/09805354  
; Publication No. US2003007875A1  
; GENERAL INFORMATION:  
; APPLICANT: Arnaout, M. Amin  
; APPLICANT: Li, Rui  
; APPLICANT: Liang, Jian-Ping  
; FILE REFERENCE: US/09/805.354  
; FILE REFERENCE: US/09/805.354  
; CURRENT APPLICATION NUMBER: US/09/805.354  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 09/758,493  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: US 60/221,950  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-805-354-4

Query Match 29.7%; Score 286.5; DB 10; Length 184;  
Best Local Similarity 33.0%; Pred. No. 4.1e-22;  
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;  
Qy 1 CPQEDSDIAPLIDGSGSIIPHDFRMKEFVSTWQKLSKTLPSLMQYSEPRHFTFK 60  
Db 1 CIXGNDLVFLFGSGNSLQDFEKFILDFMKDVKKLSNTSYQFAVQSTSYKTEFDS 60  
Qy 61 EFQNNPNSRLVKPITOLLGRTHATGIRKVVRELFTNGARKNAFKILVITDGEKFG 120



Db 61 DYVKWDPDALLKGVKRMILLTHTFGAINVATVFEVRELGARPDATKVLIIITDGE--A 118  
Qy 121 DPLGVGVIPVADREGVIRYVGVGDAPRSEKSEKQELNTIASPPRDHVPQVNNFPAKLT 180  
Db 119 TDSGNDAKD-----LIRYIIGIKGHFOTKESQETLHKPASPASEFVKILDTPEKLD 173  
Qy 181 IQNQLREK 188  
Db 174 LFTLEQKK 181

## RESULT 11

US-09-795-798-7  
; Sequence 7, Application US/09795798  
; Publication No. US20030207336A1  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/795,798  
; FILING DATE: 18-FEB-2001  
; CLASSIFICATION: Unknown  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/974,899  
; FILING DATE: Unknown  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P101481  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION CONTACT:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: Amino Acid  
; LENGTH: 184 amino acids  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 29.7%; Score 286.5; DB 11; Length 184;  
Best Local Similarity 33.0%; Pred. No. 4.1e-22;  
Matches 61; Conservative 49; Mismatches 70; Indels 7; Gaps 2;  
Qy 1 CPQSDSDIADLIDGSGIIPHDPRMKPFVSTMQLKSKTFLSLMYSEFRIHPTFK 60  
Db 1 CIKGNVDLVFLFDGNSLQDFQKILDFMKDVMKLSNTSYQFAAVQFSTVKTEFDF 60  
Qy 61 EFQNNPNRSLVPTLTOLLGRTHTATGIRKVVRELFWITNGAKNAPKILVITDGEKFG 120  
Db 61 DYVKWDPDALLKGVKRMILLTHTFGAINVATVFEVRELGARPDATKVLIIITDGE--A 118  
Qy 121 DPLGVGVIPVADREGVIRYVGVGDAPRSEKSEKQELNTIASPPRDHVPQVNNFPAKLT 180  
Db 119 TDSGNDAKD-----LIRYIIGIKGHFOTKESQETLHKPASPASEFVKILDTPEKLD 173  
Qy 181 IQNQLREK 188  
Db 174 LFTLEQKK 181

## RESULT 13

US-10-144-259-4  
; Sequence 4, Application US/10144259  
; Publication No. US20030109691A1  
; GENERAL INFORMATION:  
; APPLICANT: Arnaud, M. Amin  
; APPLICANT: Li, Rui  
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 00786-548001  
; CURRENT APPLICATION NUMBER: US/10/144,259  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: US 09/758,493  
; FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: US 60/221,950  
; FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-144-259-4

Query Match 29.7%; Score 286.5; DB 14; Length 184;  
Best Local Similarity 33.0%; Pred. No. 4.1e-22;  
Matches 62; Conservative 49; Mismatches 70; Indels 7; Gaps 2;

Query Match 29.7%; Score 286.5; DB 10; Length 184;  
Best Local Similarity 33.5%; Pred. No. 4.1e-22;  
Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;  
Qy 7 DIADLIDGSGIIPHDPRMKPFVSTMQLKSKTFLSLMYSEFRIHPTFKFQNP 66  
Db 5 DLVFLFDGNSLQDFQKILDFMKDVMKLSNTSYQFAAVQFSTVKTEFDFSVYKR 64  
Qy 67 NPSRLVKPTLTOLLGRTHTATGIRKVVRELFWITNGAKNAPKILVITDGEKFGDPLGE 126  
Db 65 DFDALLKGVKRMILLTHTFGAINVATVFEVRELGARPDATKVLIIITDGE--ATDSGNT 122  
Qy 127 DVIPVADREGVIRYVGVGDAPRSEKSEKQELNTIASPPRDHVPQVNNFPAKLTIONLR 186  
Db 123 DAKD-----LIRYIIGIKGHFOTKESQETLHKPASPASEFVKILDTPEKLDLFTLEQ 177  
Qy 187 EK 188  
Db 178 KK 179



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